What is claimed is:

1. A gene mapping method, comprising:

collecting a DNA sample from a test subjects having a characteristic of interest and control subjects;

amplifying DNA fragments from the DNA sample using a pair of forward and reverse primers which provide for amplification of nucleotide sequences of microsatellite genetic polymorphism markers located at intervals of from about 50 Kb to 150 Kb over a region of interest on the human genome, said amplifying producing DNA fragments which contain sequences of the microsatellite genetic polymorphism markers; and

statistically comparing the DNA fragments obtained from the test subject with those obtained from the control subjects;

wherein said comparing identifies DNA fragments associated with one or more genomic regions associated with the characteristic of interest.

2. The method according to claim 1, further comprising pooling the DNA samples obtained from the test subjects and pooling the DNA samples obtained from the control subjects prior to said amplifying.

3. The method according to claim 1, wherein the forward and reverse primer pairs provide for amplification of a combination of microsatellite genetic polymeric markers comprising SEQ ID NOS:1-27088.

4. The method according to claim 1, wherein analysis of the microsatellite genetic polymorphism markers is carried out using a DNA chip and a mass spectrometer.

5. A computer-readable medium carrying microsatellite polymorphic marker distribution map and one or more sequences of instructions from a user of a computer system for analyzing said markers over a desired human genomic region, wherein the distribution map comprises information regarding the position of microsatellite polymorphic markers over one or more regions of the human

genome, said markers being positioned at intervals of from about 50 Kb to 150 Kb, wherein execution of one or more sequences of instructions by one or more processors causes the one or more processor to perform a method, comprising:

receiving a query inputted by the user and receiving instructions as to a microsatellite markers or a human genomic region to include in analysis;

accessing distribution map information stored on the medium;

displaying a map showing the position of markers on a human genomic region, wherein the map provides at least the selected markers or markers within the selected region.

6. The computer-readable medium of claim 5, wherein the medium additionally carries sequence information for the markers.

7. The computer-readable medium of claim 6, wherein the sequence information comprises nucleotide sequences of SEQ ID NOS:1-27088.

8. An isolated polynucleotide useful as a primer, the polynucleotide being about 15 to 100 nucleotides in length and containing a nucleotide sequence extending in 3'-direction from the 5'-terminus of a sequence of one of SEQ ID NOS:1- 27088 or a nucleotide sequence complementary to a sequence extending in 5'-direction from the 3'-terminus of a sequence of one of SEQ ID NOS:1-27088.

9. A method of assessing susceptibility of a human subject to psoriasis vulgaris, the method comprising:

analyzing a region of about 111 kb extending from C1_2_6 to C2_4_4 for the presence a marker that is associated with psoriasis vulgaris, wherein the marker is allele 303, allele 357, allele 255, allele 259, or allele 223;

wherein detection of the marker is indicative of susceptibility of the subject to psoriasis vulgaris.

10. The method of 9, wherein the marker is allele 303.

11. The method of claim 9, wherein the subject is heterozygous and is identified as a carrier for psoriasis vulgaris.

12. The method of claim 9, wherein the subject is homozygous, and is susceptible to onset or has psorasis vulgaris.